

Figure 1

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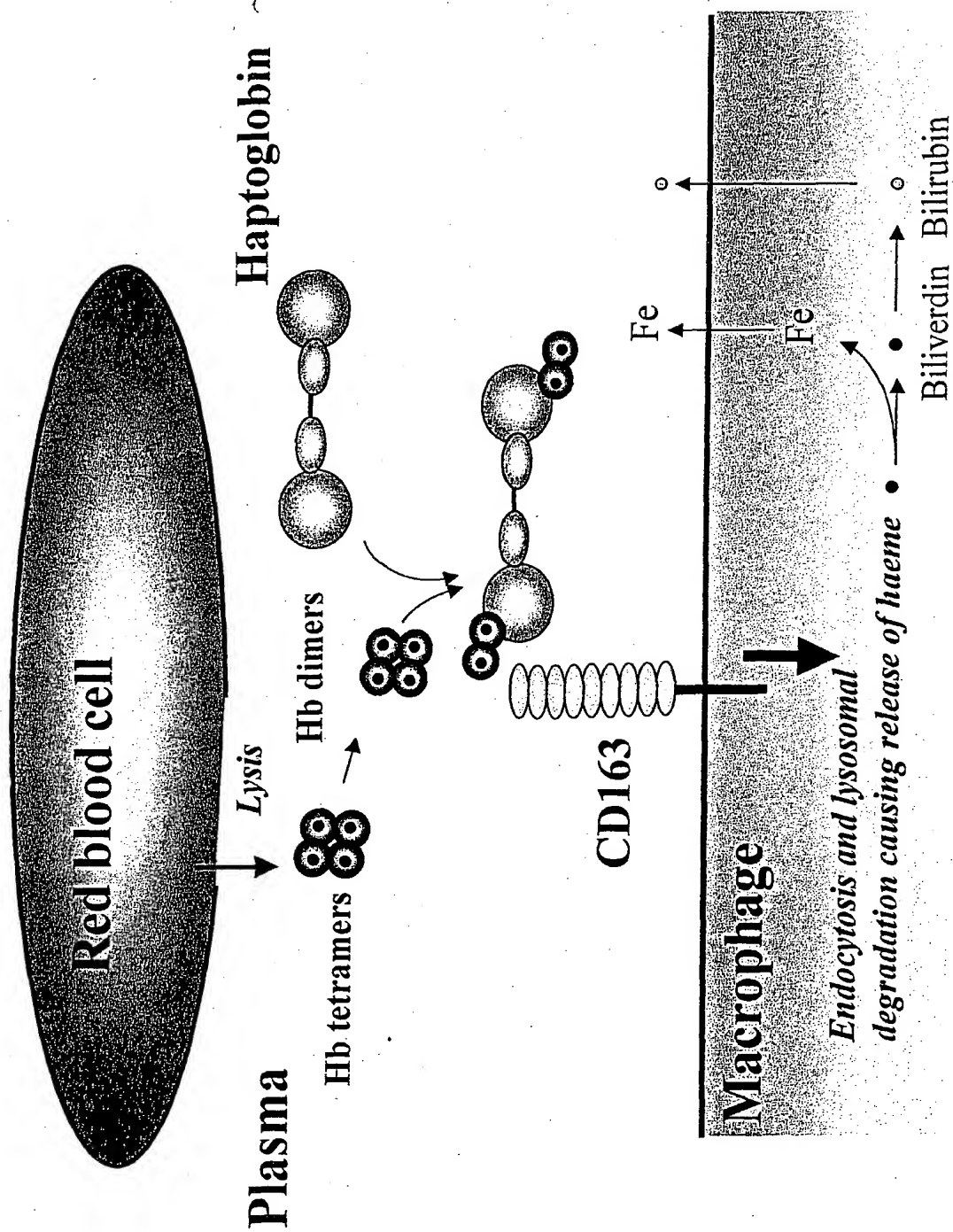


Figure 2

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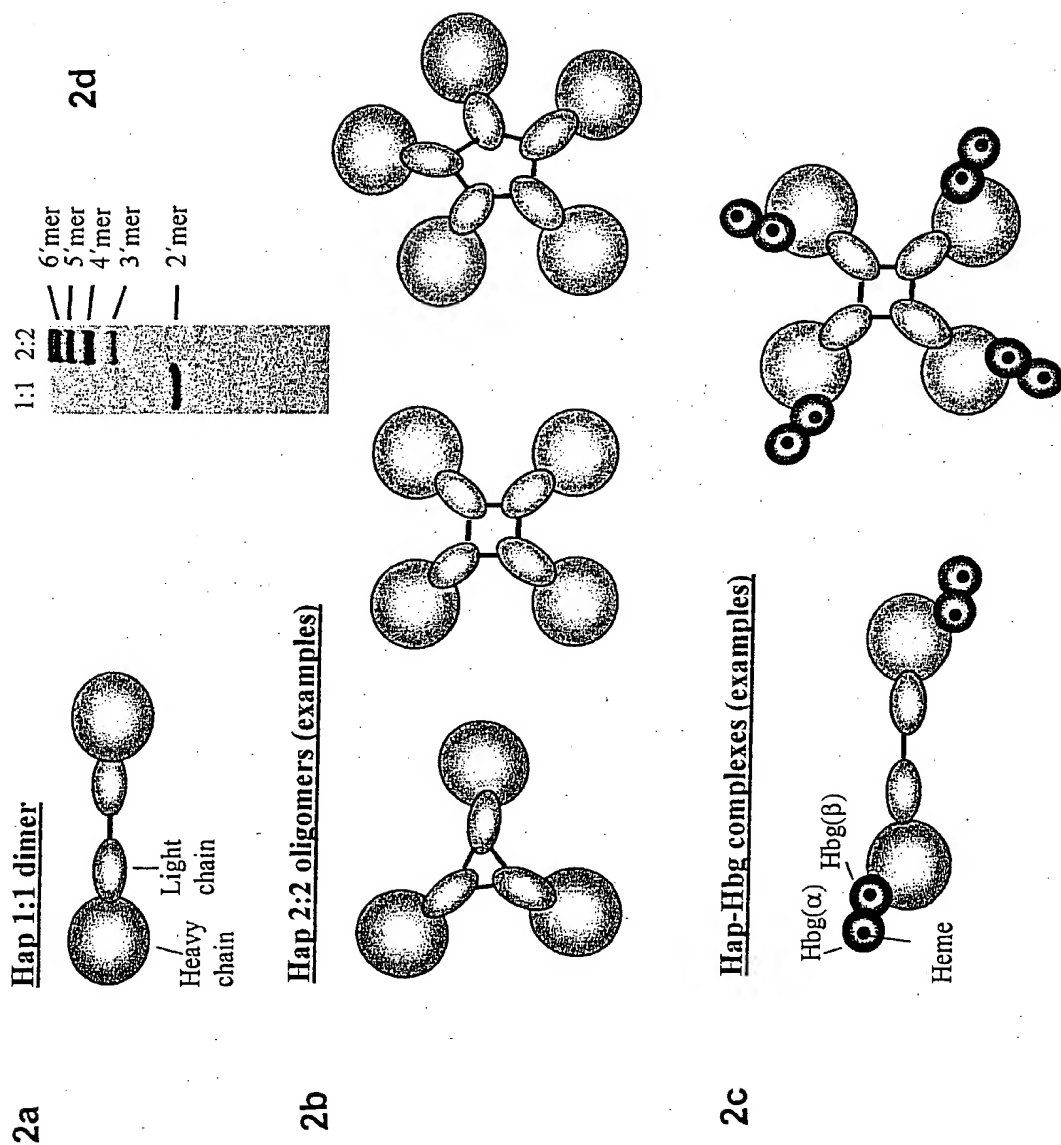


Figure 3

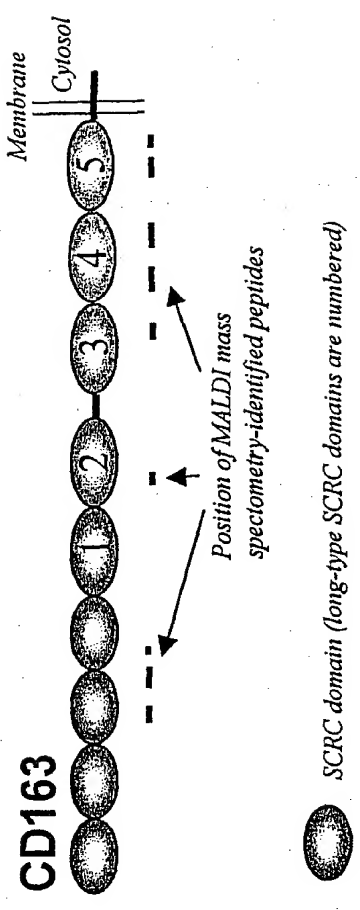


Figure 4a

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sp|P00738|HPT2_HUMAN      MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT 60
sp|P50417|HPT_ATEGE       MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIANGYVEHLVRYRCRQFYRLRA 60
tr|Q60574|Q60574         MRALGAVVTLTLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA 60
tr|Q61646|Q61646         MRALGAVVTLTLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA 60
sp|Q62558|HPT_MUSSA      MRALGAVVTLTLLWGQLFAELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRT 60
sp|P06866|HPT_RAT        MRALGAVVTLTLLWGQLFAVELGNDATDIEDDSCPKPPEIANGYVEHLVRYRCRQFYKLQT 60
tr|O35086|O35086        MRALGAVVTLTLLWGQLFAVDLSNDAMDTADDSCPKPPEIENGYVEHLVRYRC-QHYRLRT 59
sp|P19006|HPT_CANFA      -----EDTGSSEATNNTNEVSLPKPPVIENGYVEHMIROYQCKPFYKLHT 42
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sp|P50417|HPT_ATEGE       EGDGVYTLN----- 69
tr|Q60574|Q60574         EGDGVYTLN----- 69
tr|Q61646|Q61646         EGDGVYTLN----- 69
sp|Q62558|HPT_MUSSA      EGDGVYTLN----- 69
sp|P06866|HPT_RAT        EGDGIYTLN----- 69
tr|O35086|O35086        EGDGVYTLN----- 68
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sp|P50417|HPT_ATEGE       -----NEKQWINKAVGDKLPECEAVCGKPKNPANPVQRIILGGHLDAKGSFPWQAKMV 121
tr|Q60574|Q60574         -----DEKQWNTVAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
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sp|Q62558|HPT_MUSSA      -----DEKQWNTAAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
sp|P06866|HPT_RAT        -----SEKQWNPAAAGDKLPKCEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
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tr|Q60574|Q60574         SRHGLTTGATLISDQWLLTTAKNLFNLHSETASGKDIAPTTLTYVGKKNQLVEIEKVVLLHP 181
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sp|P50417|HPT_ATEGE       NYSQVDIGLIKLRQKQVSNRVMPICLPSKDYAEVGRVGYVSGWGRNANFKFTDHLKYVM 241
tr|Q60574|Q60574         NHSVVDIGLIKLRQKQVSNRVMPICLPSKDYVAPGRVGYVSGWGRNANFKFTDHLKYVM 241
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tr|O35086|O35086        NRSVVDIGVILKLRQKQVSNRVMPICLPSKDYIAPGRMGYVSGWGRNANFKFTDHLKYVM 240
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sp|P50417|HPT_ATEGE       LPVADQYQCVKHRYEGSTVPEKKTPKSPVGVQPILNEHTFCAGMSKYQEDTCYGDAGSAFA 301
tr|Q60574|Q60574         LPVADQDKCVVHYEKSTVPEKKNFTSPVGVQPILNEHTFCAGLTKEYEEDTCYGDAGSAFA 301
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Figure 4b

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sp|P50417|HPT_ATEGE       VHDLEEDTWYAAGILSFDKSCGVAEGVYVKATSIQDWVQKTIAEN 347
tr|Q60574|Q60574         IHDMEEDTWYAAGILSFDKSCAVAEGVYVRATDLKDWVQETMAKN 347
tr|Q61646|Q61646         IHDMEEDTWYAAGILSFDKSCAVAEGVYVRATDLKDWVQETMAKN 347
sp|Q62558|HPT_MUSSA       IHDMEEDTWXAAGILSFDKSCAVAEGVYVRATDLKDWVQETMAKK 347
sp|P06866|HPT_RAT         VHDTEEDTWYAAGILSFDKSCAVAEGVYVKATDLKDWVQETMAKN 347
tr|O35086|O35086         IHDLEQDTWYAAGILSFDKSCSVAEGVYVKVNSFLDWIQETMAKN 346
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Figure 5a

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CD163 MVLLLEDSGSADFRRHFNLS PFTITVVLILLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60  
 CD163 cyt. Var 1 MVLLLEDSGSADFRRHFNLS PFTITVVLILLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60  
 CD163 cyt. var 2 MVLLLEDSGSADFRRHFNLS PFTITVVLILLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60  
 CD163 ext. cell. Var. MVLLLEDSGSADFRRHFNLS PFTITVVLILLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60  
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 tr|Q07900|Q07900 ALWDCKHDGWGKHSNCTHQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVC 180  
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 tr|Q07900|Q07900 -----RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST 627  
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 \*\*\*\*\*

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Figure 5b

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tr|Q07898|Q07898 PGGARFGKGNQIWRHMFHCTGTEQHMGDPCVTALGASLCPSEQVASVICSGNQSQTLSS 687  
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tr|Q07900|Q07900 PGGARFGKGNQIWRHMFHCTGTEQHMGDPCVTALGASLCPSEQVASVICSGNQSQTLSS 687  
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tr|Q07899|Q07899 AHVVCRLGCGEAINATGSAHFEGGTGPIWLDEMKNCGKESRIWQCHSHGWGQQNCRHKE 807  
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tr|Q07901|Q07901 DAGVICSEFMSLRLTSEASREACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCA 900  
tr|Q07900|Q07900 DAGVICSEFMSLRLTSEASREACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCA 867  
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tr|Q07900|Q07900 GKINPASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEETWITCDNKIRLQ 927  
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\*\*\*\*\*

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\*\*\*\*\*

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Figure 6a

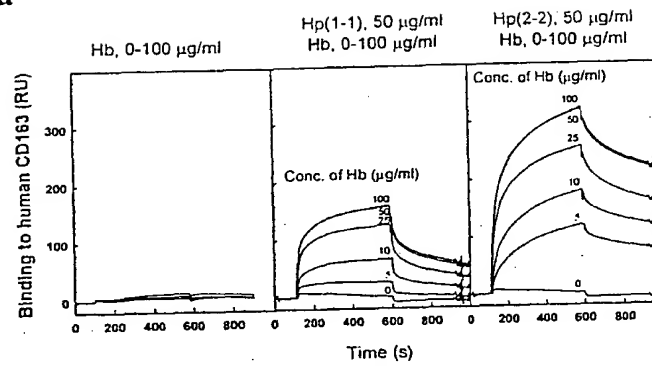


Figure 6b

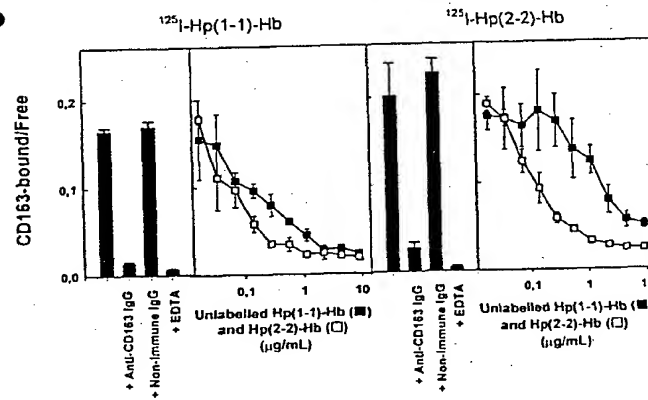




Figure 7a

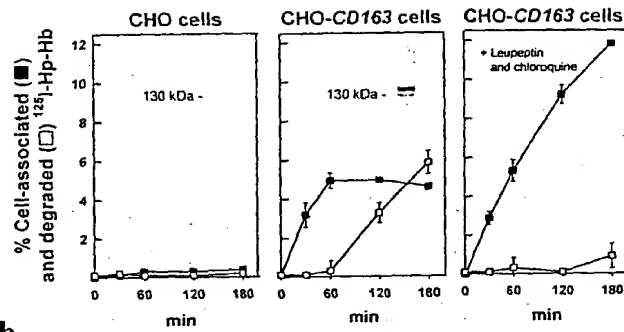


Figure 7b

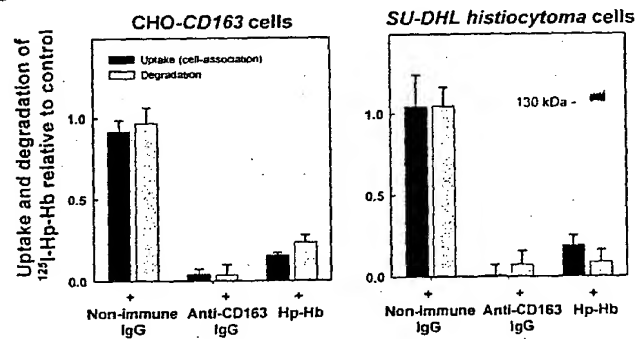
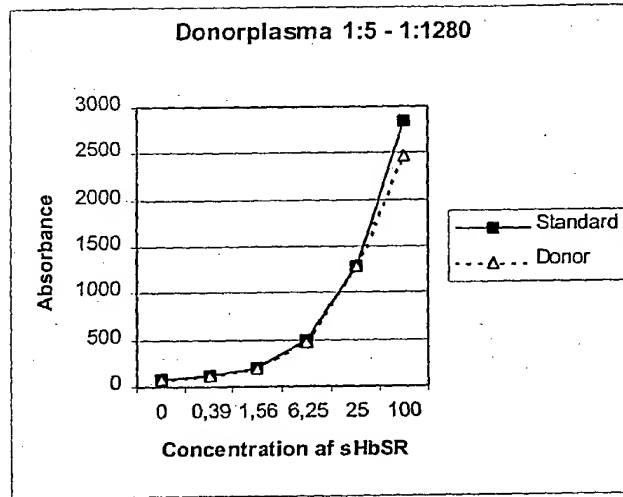


Figure 8



T09701-15/2660

# Uptake of Alexa Flour 488-labeled Hp-Hb in CHO cells expressing HbSR

Fig. 9b

Cubilin-transfected  
CHO cells (controls)

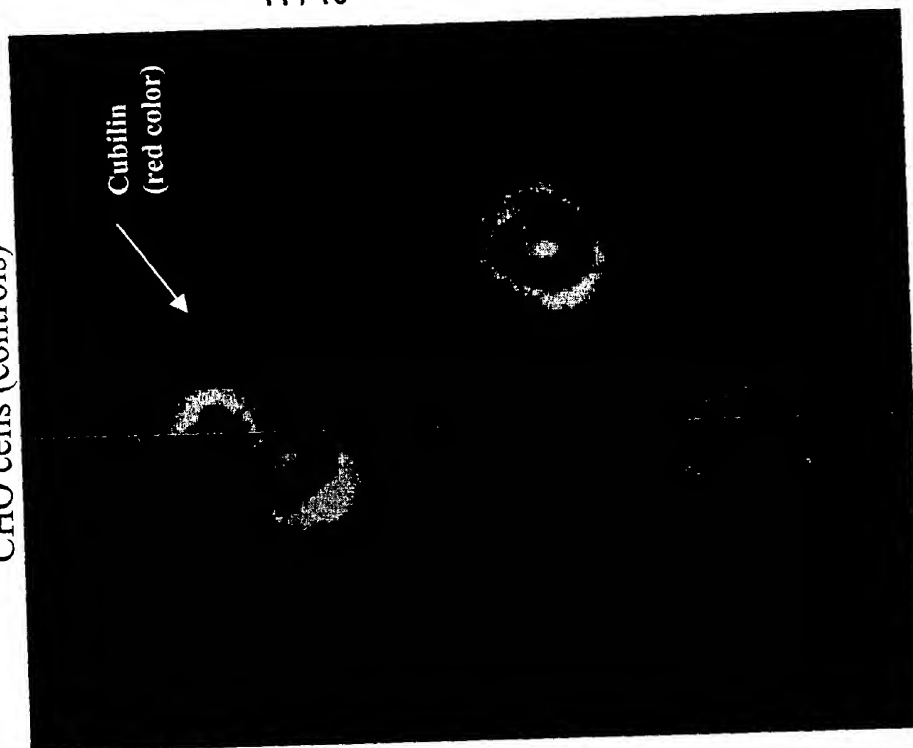
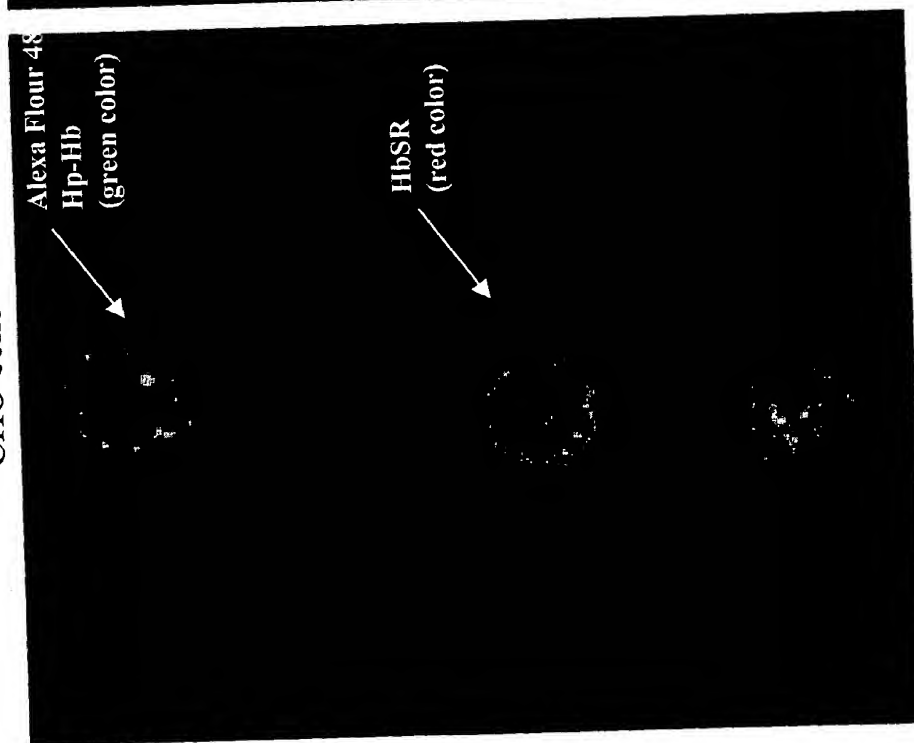


Fig. 9a

HbSR-transfected  
CHO cells



**Fig. 10**

Binding of Hp(1-1)-Hb to immobilized HbSR purified from placenta or recombinant HbSR derivative corresponding to SRCR domain 1-6

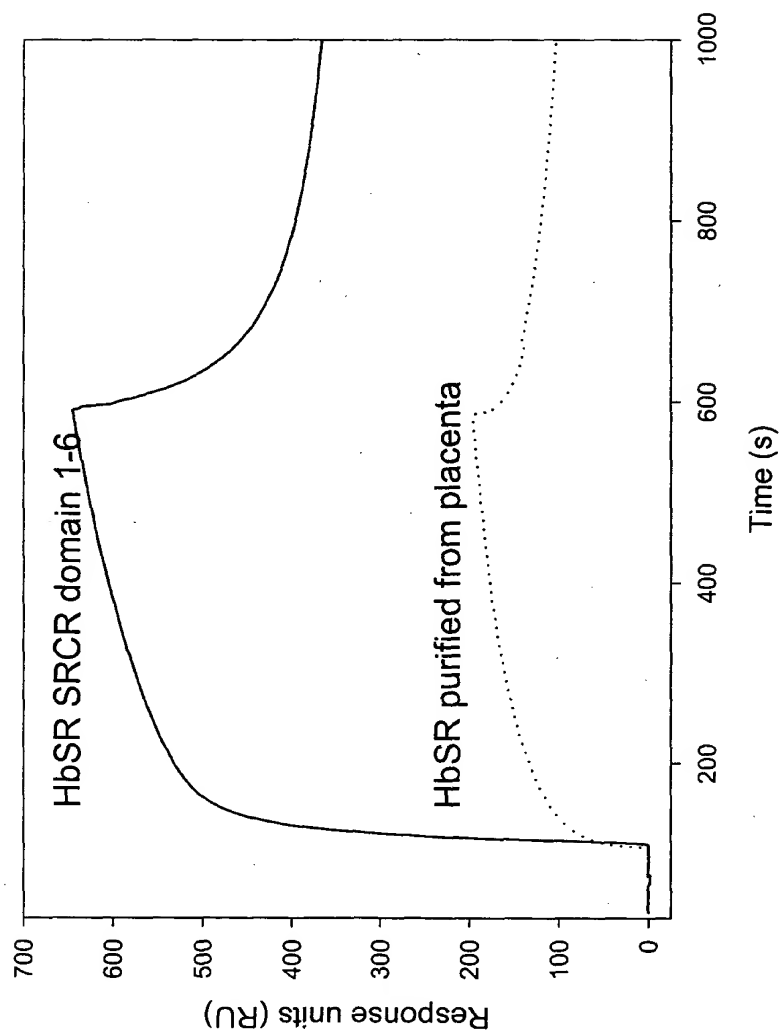


Fig. 11

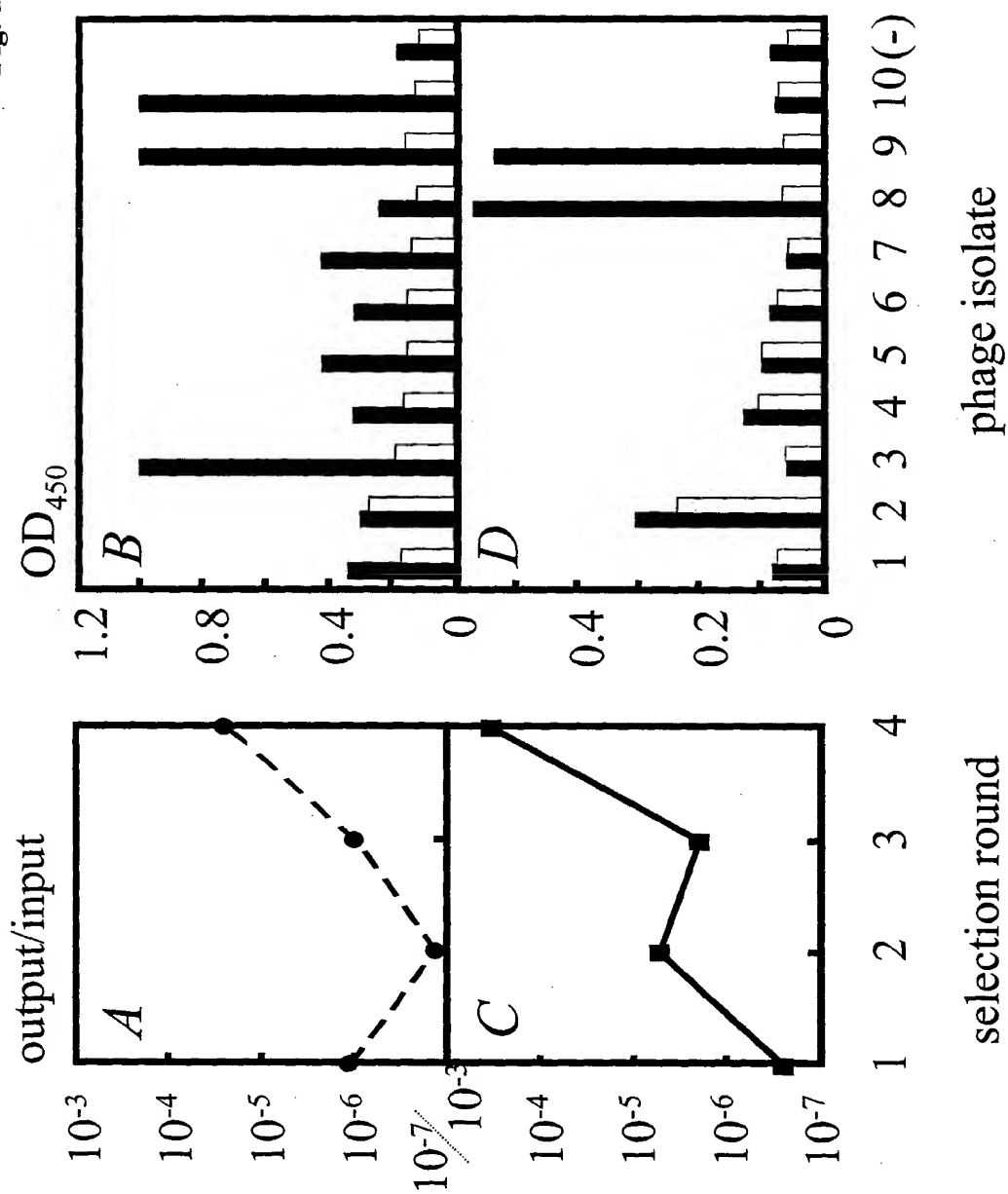
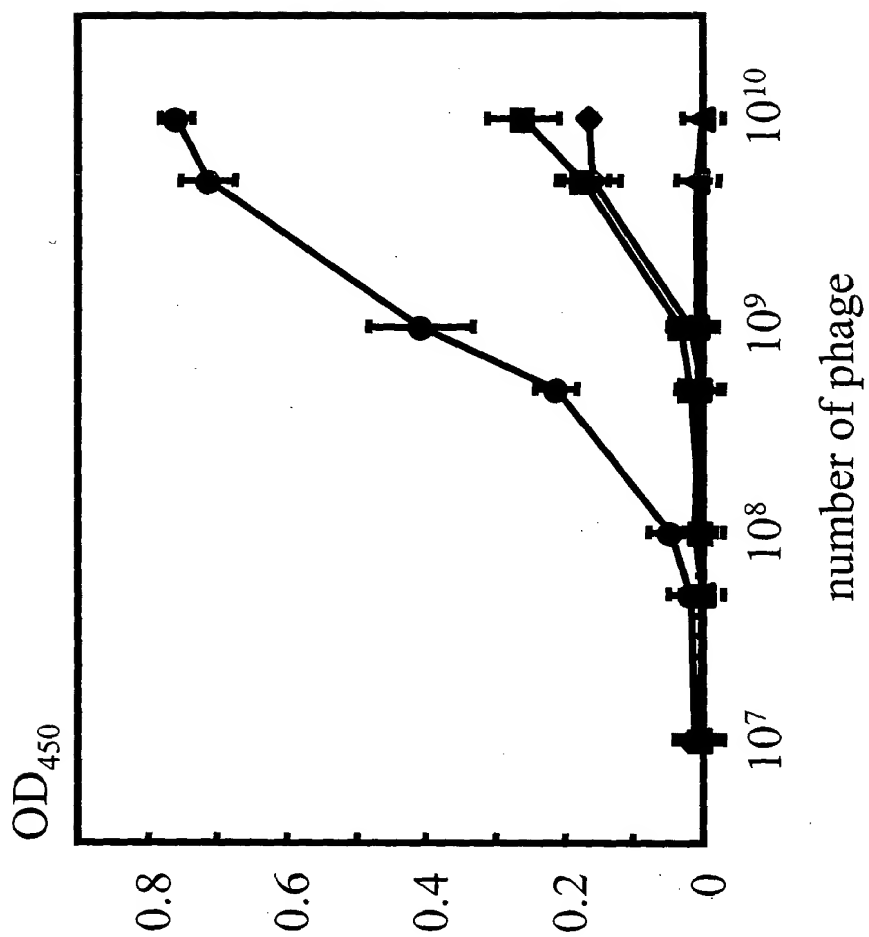


Fig. 12a



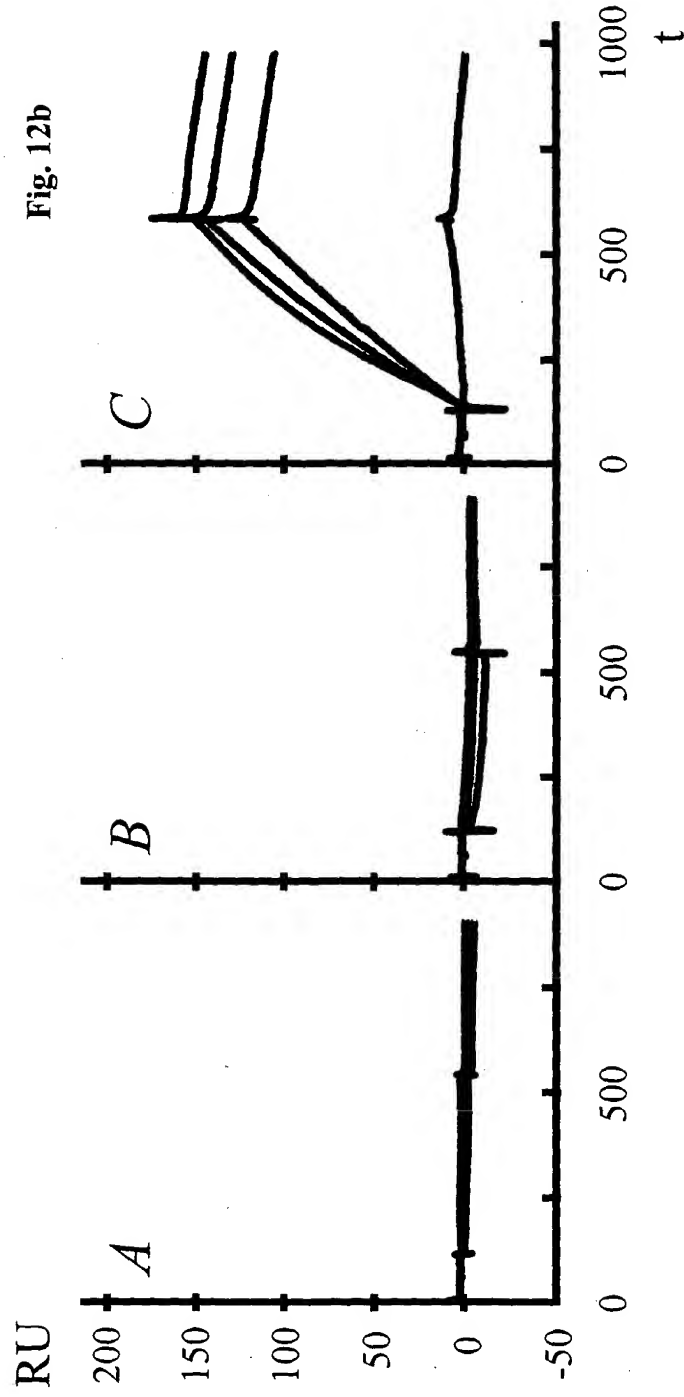


Fig. 13

